

				GenCore version 5.1.3
Copyright	(c) 1993 - 2002	CompuGen Ltd.		
OM nucleic - nucleic search, using sw model				
Run on:	November 30, 2002, 10:08:33 ; Search time 2532 Seconds			
Scoring table:	IDENTITY_NUC	(without alignments)		
Gapop	10.0 , Gapext 1.0			
Searched:	16154066 seqs, 8097743376 residues			
Post-processing:	Minimum Match 0%			
Maximum DB seq length:	0			
Minimum DB seq length:	0			
Total number of hits satisfying chosen parameters:	32308132			
Maximum DB seq length:	200000000			
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing-first 45 summaries				
Database:	EST*			
1: em_estba:*	c	7	553.6	20.0
2: em_estbun:*	c	8	516	18.7
3: em_estin:*	c	9	416.4	15.1
4: em_estmu:*	c	10	407.8	14.7
5: em_estov:*	c	11	407.4	14.7
6: em_estpl:*	c	12	372.8	13.5
7: em_estro:*	c	13	368.2	13.3
8: em_htc:*	c	14	361.8	13.1
9: gp_est1:*	c	15	359.8	13.0
10: qb_est2:*	c	16	359	13.0
11: qb_htc:*	c	17	345	12.5
12: qb_est3:*	c	18	338.2	12.2
13: qb_est4:*	c	19	320	11.6
14: qb_est5:*	c	20	319.8	11.6
15: em_estom:*	c	21	310	11.0
16: qb_gss:*	c	22	295.8	10.7
17: qb_gss_inv:*	c	23	294.2	10.6
18: em_gss_hum:*	c	24	291.4	10.5
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20: em_gss_pln:*	c	26	267.2	9.7
21: em_gss_vrt:*	c	27	261	9.4
22: em_gss_fun:*	c	28	258.8	9.4
23: em_gss_mam:*	c	29	257.8	9.3
24: em_gss_mus:*	c	30	253.8	9.2
25: em_gss_other:*	c	31	240.6	8.7
26: em_gss_pro:*	c	32	237.8	8.6
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		c	35	213.6
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		c	38	206.2
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		c	43	193.8
		c	44	189.2
		c	45	187.8
				AL286344 Tetraodon
				BG910325 60380592
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				BL3349372 CH30-32M
				BC023215 Homo sapi
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				AI265769 Tetraodon
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				AI330949 Tetraodon
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				BS371210 dac13d12
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				AL333730 Tetraodon
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				AA733833 vv0f02.r
				AI297156 Tetraodon
				ALIGNMENTS
RESULT	1			
B1913344				
LOCUS	B1913344	8087 bp mRNA	linear	EST 16-OCT-2001
DEFINITION	60317823F1 NIH_MGC_121 Homo sapiens	CDNA clone IMAGE:5243308	5',	
mRNA Sequence.				
ACCESSION	B1913344			
VERSION	GI:16177710			
KEYWORDS	EST.			
SOURCE	human,			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 887)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D.			
	Email: cgabs-r@mail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LILN at:			
	http://image.llnl.gov			
	Plate: LLM163 row: m column: 05			
	High quality sequence stop: 782.			
	Location/Qualifiers			
	source			
	1 . .887			
	SUMMARIES			
Result	Query	Match Length	DB ID	Description
No.	Score			
1	813.8	29.4	887 13	B1913344 60317823
2	743.4	26.9	791 13	B1523145 603175911
3	739.8	26.7	792 13	B1522813 603175911
4	673.2	24.3	775 14	BQ770745 UTM-FIO-
5	657	23.8	665 14	BQ189572 UTE-EJ1-
6	560.2	20.3	676 10	BB280958 BB280958

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



source
Oy 2018 CGGTGGACAACTGTCAGAAGACANACCTGCCCTGGTGGGACCCATTCTGGA 2077
Db 611 CGGTGGACAACTGTCAGAAGACAAACUCCGGCCTGCTGGGACCCATTCTGGA 552
Oy 2078 GGAGACCAGTCACTGGAGGCCATCACCGTCAGTGACAGGGATGAGGATGAAT 2137
Db 551 GGAGACCAGTCACTGGAGGCCATCACCGTCAGTGACAGGGATGAGGATGAAT 495
Oy 2138 CGGGGAGGAGGGCAGGCCACTCTGCTTGACTACATGCCACTCTGACTGTGCT 2197
Db 494 CGGGGAGGAGGGCAGGCCACTCTGCTTGACTACATGCCACTCTGACTGTGCT 435
Oy 2258 CGGTGTCATCCTCATCATGGCATGTCACGGCCATCATGGGACCTGGCCTGCT 2317
Db 374 CGGTGTCATCCTCATCATGGCATGTCACGGCCATCATGGGACCTGGCCTGCT 315
Oy 2318 TCGGCCTGACCACTTGSGTCTCAAGATTCAGTCATGTCACASCTGTTTGTGCTGCAATTGGCA 2377
Db 314 TCGGCCTGACCACTTGSGTCTCAAGATTCAGTCATGTCACASCTGTTTGTGCTGCAATTGGCA 255
Oy 2378 CCTCTGTCAGAACATACCTTGCCAGCAAGCTGCTGCCCTCAGGATGATAGCAGAC 2437
Db 254 CCTCTGTCAGAACATACCTTGCCAGCAAGCTGCTGCCCTCAGGATGATAGCAGAC 195
Oy 2438 CCTCCATTTGGACACGTCAGGACAGGGCAGCACCGGCTCAATGCTCTCCGGCAGTCGGCTGG 2497
Db 194 CCTCCATTTGGACACGTCAGGACAGGGCAGCACCGGCTCAATGCTCTCCGGCAGTCGGCTGG 135
Oy 2498 CCTGGGTCGGCCGCGCCTCATCTCTGGCTCAGGGACAGGAGTCCACCGTGTGCGCC 2557
Db 134 CCTGGGTCGGCCGCGCCTCATCTCTGGCTCAGGGACAGGAGTCCACCGTGTGCGCC 75
Oy 2558 GCAACTGGCTTCGTCACCCCTCACCATCTTGCAATTGCTGCTGCAAGCGTG 2616
Db 74 GCACACTGGCTTCGTCGTCACCCCTCACCATCTGCTGCAATTGCTGCAAGCGTG 15
Oy 2617 CTCTGTACCGAG 2630
Db 14 CTCTGTACCGAG 1
BASE COUNT
202 a
179 c
227 g
184 t
ORIGIN
Query Match 26.7%; Score 739.8; DB 13; Length 792;
Best Local Similarity 98.7%; Pred. No. 1.2e-185; Matches 767; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
Matches 767; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
Oy 993 CTTAGATTCAGCGTGGAGATGCCATTACTATGCTCTTCCACCAAACAGAGCCG 1052
Db 1 CTTAGATTCAGCGTGGAGATGCCATTACTATGCTCTTCCACCAAACAGAGCCG 60
Oy 1053 CGCTTCTTACCGTATCCAAGCCACTCTGTTATGACTGACTGTTGGGAGGCAATATCTGAGAA 1112
Db 61 CGCTTCTTACCGTATCCAAGCCACTCTGTTATGACTGACTGTTGGGAGGCAATATCTGAGAA 120
Oy 1113 ACATGACAGACAAGCAAGCCAAAGAGGCTCCAGCATAGCGAGGTCAACCGATGAGCC 1172
Db 121 ACATGACAGACAAGCAAGCCAAAGGAGGCTCCAGCATAGCGAGGTCAACCGATGAGCC 180
Oy 1173 TGGGACTTACCTGACAGTGTGAGGAAAGGGAGACATGTCAGAACGATGAGT 1232
Db 181 TGAGGACTTATTTCCAGGTCTCTTGACCATGTTCTACAGTCCTGAGACTG 240
Oy 1233 TGGGCTTACCTGACAGTGTGAGGAAAGGGAGACATGTCAGAACGATGAGT 1292
Db 241 TGGGCTTACCTGACAGTGTGAGGAAAGGGAGACATGTCAGAACGATGAGT 300
Oy 1293 GGACTACAAACAGGGTGGTCTGCCAATOCAGGGCTGACTATGAGTCACAGGG 1352
Db 301 GGACTACAAACAGGGTGGTCTGCCAATOCAGGGCTGACTATGAGTCACAGGG 360
Oy 1353 CAGGGTGGTCTGAGAGGCCAGGGAGACCCAGGAGGACTCTCGTSGGCATATTGAGA 1412
Db 361 CAGGGTGGTCTGAGAGGCCAGGGAGACCCAGGAGGACTCTCGTSGGCATATTGAGA 420
Oy 1413 CGACATTGAGGGATGAAACACTCTTGTAGGTGAGCACTCCGATAGAGA 1472
Db 421 CGACATTGAGGGATGAAACACTCTTGTAGGTGAGCACTCCGATAGAGA 480
Oy 1473 GGAGCAGGAGGGATGCCAATATCACAGCTCTCCCTGGGC 1532
Db 481 GGAGCAGGAGGGATGCCAATATCACAGCTCTCCCTGGGC 540
Oy 1533 TGGCTTACCTGCCCTTGTCAGGAGTACATCTTGTAAAGTGACATGCCATAGAGA 1592
Db 541 TGGCTTACCTGCCCTTGTCAGGAGTACATCTTGTAAAGTGACATGCCATAGAGA 600
Oy 1593 CTCACTTTGATGATGACTATTCAGTCAGTGAGGATATGGGTTATGGAGCTAA 1652
Db 601 CTCACTTTGATGACTATTCAGTCAGTGAGGATATGGGTTATGGAGCTAA 660
Oy 1653 GGTCTGGGACATCAGTGGCCAGTACCATCTGGAGATGACCATGAGTAGAG 1711
Db 661 GGTCTGGGACATCAGTGGCCAGTACCATCTGGAGATGACCATGAGTAGAG 720
Oy 1712 GGACGCCAAGGGTGGGGT - GAGGACTTCAAGACACATATGGGAGTGAAT 1766
FEATURES
High quality sequence stop: 778.
Location/Qualifiers

RESULT 4	BQ770745	775 bp mRNA linear EST 26-JUL-2002	303
LOCUS	BQ770745	UI-M-F10-byw-c-07-0-UI_r1 NIH_BMAP_F10 Mus musculus cDNA clone IMAGE:600062 5', mRNA sequence.	303
DEFINITION	BQ770745	EST.	303
ACCESSION	BQ770745.1	GI:21979219	303
VERSION			303
KEYWORDS	house mouse.		303
ORGANISM	Mus musculus		303
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 775) NIH_MGIC http://mgic.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa DNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: http://image.lnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: PYX-5' Location/Qualifiers 1..775 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:640062" /clone_id="NIH_BMAP_F10" /tissue_type="whole brain" /dev_stage="embryo 12.5dpc" /lab_host="DHLB (T1 phage resistant)" /note="Organ: Brain; Vector: PYX- Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-ASC vector. The library tag sequence located between the Not I site and the polyA tail is GAGCCCGAC. This library was created for the University of Iowa Brain Anatomy Project (BMAP); "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator." BASE COUNT 168 a 185 c 202 g 219 t 1 others ORIGIN Matches 711; Conservative 0; Mismatches 64; Indels 0; Gaps 0;	303	
RESULT 4	BQ770745	775 bp mRNA linear EST 26-JUL-2002	303
LOCUS	BQ770745	UI-M-F10-byw-c-07-0-UI_r1 NIH_BMAP_F10 Mus musculus cDNA clone IMAGE:600062 5', mRNA sequence.	303
DEFINITION	BQ770745	EST.	303
ACCESSION	BQ770745.1	GI:21979219	303
VERSION			303
KEYWORDS	house mouse.		303
ORGANISM	Mus musculus		303
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 775) NIH_MGIC http://mgic.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa DNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: http://image.lnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: PYX-5' Location/Qualifiers 1..775 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:640062" /clone_id="NIH_BMAP_F10" /tissue_type="whole brain" /dev_stage="embryo 12.5dpc" /lab_host="DHLB (T1 phage resistant)" /note="Organ: Brain; Vector: PYX- Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-ASC vector. The library tag sequence located between the Not I site and the polyA tail is GAGCCCGAC. This library was created for the University of Iowa Brain Anatomy Project (BMAP); "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator." BASE COUNT 168 a 185 c 202 g 219 t 1 others ORIGIN Matches 711; Conservative 0; Mismatches 64; Indels 0; Gaps 0;	303	
RESULT 5	BQ189572	665 bp mRNA linear EST 30-APR-2002	304
LOCUS	BQ189572	UI-E-E1-aka-f-22-0-UI_r1 UI-E-E1 Homo sapiens cDNA clone IMAGE:600062 5', mRNA sequence.	304
DEFINITION	BQ189572	EST.	304
ACCESSION	BQ189572	GI:20365123	304
VERSION			304
KEYWORDS	human.		304
ORGANISM	Homo sapiens		304
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 665) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery. Genome Res. 6 (9), 791-806 (1996) Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Echiststein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Tissue Procurement: Dr. Gregg Hageman DNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research	304	

FEATURES	Seq primer: M13 REVERSE.	Genetics (www.reagen.com).
source	Location/Qualifiers	
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/note="Organ: eye; Vector: pMT73-pac (Pharmacia) with a modified polylinker; Site-1: EcoR I; Site-2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares. Genome Research, 6:791-805, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pMT73-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATGAAA ; lens, CGATTACGA; eye anterior segment, ATGCCCAT; optic nerve, CCATTAGCG; retina, CGCGC; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the visual system, supported by National Eye Institute (NEI)."		
BASE COUNT		
127 a 198 c 179 g	161 t	
Query Match	23.8%; Score 657; DB 14; Length 665;	
Best Local Similarity	99.2%	
Matches	60: Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Qy	1964 GTGAACACCCAACTAGAACATGAGACTCATGAGAGACTATGAGTCAGAACATCGGTG 2023	Qy 2504 CCGTGCCCCGCATCTACTGGCTCTGCAGGACAGGAGTCCACG 2563
Db	1 GTGACACCCCAACTAGAACATGAGACTCATGAGAGACTATGAGTCAGAACATCGGTG 60	Db 541 CGGTGGCCGATCTACTGGCTCTGCAGGACAGGAGTCCACG 600
Qy	2024 ACAAATGATCAAGAGAACCTGGCTTGTGTTGGGACCCATTCCCTGGAGGACC 2083	Qy 2564 TGGCTCTTCGGTACCCCTCACATTTGAGTTGCTGATCGCATCACGGCTT 2623
Db	61 ACAAACTGATCAAGAGAACCTGGCTTGTGTTGGGACCCATTCCCTGGAGGACC 120	Db 601 TGGCCCTTCGGTACCCCTCACATTTGAGTTGCTGATCGCATCACGGCTT 660
Oy	2084 AGTCATGGGCCATCACCGTAGTCAGGACAGGGATGAGGATGAGGATGATCGGGG 2143	Oy 2624 ACCGA 2628
Db	121 AGTCATGGGCCATCACCGTAGTCAGGACAGGGATGAGGATGAGGATGATCGGGG 180	Db 661 TACGA 665
Qy	2144 AGGAGAGGCTCCCCTCTGCTTGTACTAGTCATGACTCTGACTCTGCTCTGGAGG 2203	RESULT 6
Db	181 AGGAGAGGCTCCCCTCTGCTTGTACTAGTCATGACTCTGCTCTGGAGG 240	BB280958
Qy	2204 TGTCTGTTGGCTGTGTCGGCCACAGAGTACTGGCACCGGCTGGCTCTGGCT 2263	BB280958 RIKEN full-length enriched, adult retina Mus musculus mRNA clone A970029A02 3', similar to U53420 Rattus norvegicus sodium-calcium exchanger form 3 (NCX3) mRNA, mRNA sequence.
Db	241 TGTCTGTTGGCTGTGTCGGCCACAGAGTACTGGCACCGGCTGGCTCTGGCT 300	BB280958 2 GI:15411103
Oy	2264 CCATCCTCATCATGGCATGCTACGGCCATCTGGCTCTGGCTCTGGCT 2323	ACCESSION
Db	301 CCATCCTCATCATGGCATGCTACGGCCATCTGGCTCTGGCTCTGGCT 360	VERSION
Qy	2324 GCACCATGGCTCAAGATGTCAGTCAGCTCACAGCTGTTGGCTGGGATTCGGCTCTG 2383	KEYWORDS
Db	361 GCACCATGGCTCAAGATGTCAGTCAGCTGTTGGCTGGGATTCGGCTCTG 420	SOURCE
Qy	2384 TCCCGATACCTTGGCAGAACAGCTGCTCCAGGAGTATATGCAAGCGCTCCA 2443	ORGANISM
Db	421 TCCCGATACCTTGGCAGAACAGCTGCTCCAGGAGTATATGCAAGCGCTCCA 480	Mus musculus
Qy	2444 TTGGCAACGTCAGGCGCAGAACGGCTCAATGCTCTCCGGCTGGCTGT 2503	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Db	481 TTGGCAACGTCAGGCGCAGAACGGCTCAATGCTCTCCGGCTGGCTGT 540	REFERENCE
		Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,I., Orido,T., Saito,R., Sakai,C., Tagami,M., Tezuka,A., Shiraki,T., Sogabe,Y., Suzuki,H., Muramatsu,M. and Hayashizaki,Y., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y., RIKEN Mouse EGTS (Arakawa,T., et al. 2001)
		TITLE
		JOURNAL
		COMMENT
		Unpublished (2001)
		On Jul 9, 2000 this sequence version replaced gi:8981407.
		Contact: Yoshihinde Hayashizaki
		Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Sheihiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayashizaki,Y., Muramatsu,M. and Hayashizaki,Y., M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. , 10 (10), 1617-1630 (2000) wagi,K., Fujikake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuo ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. Genome Res. , 11 (2), 281-289 (2001) Yamamoto,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Alzawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001) Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken. Genomic Sciences Center and Genome Science Laboratory in Riken.





RESULT 9				
BT1756778	718 bp	mRNA	linear	EST 25-SEP-2001
LOCUS	BT1756778	603024449FL NIH_MGC_114	Homo sapiens	cDNA clone IMAGE:5194668 5'
DEFINITION				mRNA sequence.
ACCESSION				BT1756778
VERSION				BT1756778.1
KEYWORDS				EST.
SOURCE				human.
ORGANISM				<i>Homo sapiens</i>
REFERENCE				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.
AUTHORS				1. (bases 1 to 718)
TITLE				NIH-MGC <a href="http://mgc.ncbi.nlm.nih.gov/">http://mgc.ncbi.nlm.nih.gov/</a>
JOURNAL				National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT				Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
TISSUE				Procurement: Life Technologies, Inc.
PROCUREMENT				Library Preparation: Life Technologies, Inc.
CNA				Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA				Sequencing by: Incyte Genomics, Inc.
Clone distribution:				MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
source				http://1Image.llnl.gov
FEATURES				High quality sequence stop: 644.
source				Location/Qualifiers 1. -718
source				/clone_id="NIH_MGC_114" /lab_host="DH10B" /db_xref="IMAGE:5194668" /organism="Homo sapiens"
Site_2:				ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library.
BASE COUNT	187	a 162	c 219	t 9 150
ORIGIN				
Query Match	15.1%			Score 416.4; DB 13; Length 718;
Best Local Similarity	94.8%			Pred. No. 1.8e-99;
Matches	474;			Conservative 0; Mismatches 21; Indels 5; Gaps 4;
y	1887			AGATGCTGACAGACAGAAGACTGCTGATGGAGAGAGGGCCAGAGATACGAGAT 1946
Db	215			AGATGCTGACAGACAGAAGACTGCTGATGGAGAGGGCCAGAGATACGAGAT 274
Qy	1947			GGGAAGCCAGTTGGTGAAACGCCAACATAGAACGTCATATTGAGAGCTCTGA 2006
Db	275			GGGAAGCCAGTTGGTGAAACGCCAACATAGAACGTCATATTGAGAGCTCTGA 334
Qy	2007			GTCAGACTACCGTGGACAACATGATCAGAAGACAACTGGCTTGTGGAC 2066
Db	335			GTCAGACTACCGTGGACAACATGATCAGAAGACAACTGGCTTGTGGAC 394
Qy	2067			CCATTCCTGGAGGACACTCTGGAGGCCATACCGTCAGTCAGGGATGAGGA 2126
Db	395			CCATTCCTGGAGGACACTCTGGAGGCCATACCGTCAGTCAGGGATGAGGA 454
Qy	2127			TGAGTGTCTGGAGGGCTGTGCTGGCGTGGCCGCCACAGAGTACTGGCACGCT 2186
Db	455			TGAGTGTCTGGAGGGCTGTGCTGGCGTGGCCGCCACAGAGTACTGGCACGCT 513
Qy	2187			GACGTCTCTGGAGGGCTGTGCTGGCGTGGCCGCCACAGAGTACTGGCACGCT 2246
Db	514			GACGTCTCTGGAGGGCTGTGCTGGCGTGGCCGCCACAGAGTACTGGCACGCT 573
RESULT 10				
BF190598	475 bp	mRNA	linear	EST 02-NOV-2000
LOCUS	BF190598	237175	MARC 2PIG	Sus scrofa cDNA 5', mRNA sequence.
DEFINITION				BR190598
ACCESSION				BR190598.1
VERSION				GI:11073967
KEYWORDS				EST.
SOURCE				pIG.
ORGANISM				<i>Sus scrofa</i>
REFERENCE				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
AUTHORS				1. (bases 1 to 475)
TITLE				Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grossie,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
JOURNAL				Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
COMMENT				Unpublished (2000)
source				Contact: Smith TPL
source				USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
source				Email: smith@email.marc.usda.gov
source				Single pass sequencing. Bases called and alt. trimmed with phred v0.980504.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRIMERS				FORWARD: AGRAAACGCTAGACCAT BACKWARD: GTTTCCACGACGACG Plate: 64 row: H column: 12 Seq primer: ATTTGGTGCACATAG Location/Qualifiers 1. .475
FEATURES				/organism="Sus scrofa" /db_xref="IMAGE:9823" /clone_id="MARC 2PIG" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT	68	a 161	c 131	t 9 115
ORIGIN				
Query Match	14.7%			Score 407.8; DB 12; Length 475;
Best Local Similarity	91.2%			Pred. No. 2.7e-97;
Matches	433;			Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy	2261			TCTCCATCCATCATCATGGCATGTCAGGCCATCATGGGGACCTGGCCCTCCACTCG 2320
Db	1			TCTCCATCCATCATCATGGCATGTCAGGCCATCATGGGGACCTGGCCCTCCACTCG 60
Qy	2321			GCTGCCACCATGGCTCAAGATTCAGTCACAGCTGTTGTTGTCGCACTGGCACCT 2380
Db	61			GCTGCCACCATGGCTCAAGATTCAGTCACAGCTGTTGTTGTCGCACTGGCACCT 120
Qy	2381			CTGTCGACGATAGCTGGCAGAACAGTCTGCTGCCCTCCAGGATGATATGGAGACGCC 2440

		Query Match	14.7%	Score 407.4;	DB 17;	Length 499;
QY	2441	CATTGGCAACCTGTGACGGCAGAACCGCGCTGAATGTTCTGGCATCGCCCTGGCT	2500	Best local Similarity 91.3%;	Pred. No. 3.5e-97;	
Db	181	CCATTGGCAACCTGTGACGGCAGAACCGCGCTGAATGTTCTGGCATCGCCCTGGCT	240	Matches 454; Conservative 0;	Mismatches 41;	Indels 2;
QY	2501	GCGCCGGGCCCATCTACTGGCTTCGGAGGACAGGCTCCACGTGCGGCCCTGGCT	2560	Gaps 2;		
Db	241	GCGTGTGGCCGCATCTACTGGCTTCGGAGGACAGGCTCCACGTGCGGCCCTGGCT	300			
QY	2561	CACTGGCCTTCGGTACCCCTTCACCATCTTGATTGTCATCACCGTGCT	2620			
Db	301	CCTGGCCTTCGGTACCCCTTCACCATCTTGATTGTCATCACCGTGCT	360			
QY	2621	TGTACCCGAGGGGCCGACCTGGAGGGACTTGGTGGCCCGGCGCTCAAGCTCG	2680			
Db	361	TGTACCCGAGGGGCCGACCTGGTGGCCGAGCTGGGGCCCTGCGGCTCAAGCTCG	420			
QY	2681	CCACACATGGCTTGTGAGGCTGTCCTCATACATCTTGCCACACT 2735				
Db	421	CCACACTGGCTTGTGAGGCTGTCCTCATACATCTTGCCACACT 475				
RESULT 11						
BH349372/C						
LOCUS	BH349372	499 bp	DNA	linear	GSS 03-DEC-2001	
DEFINITION	CH230-32M17-TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone					
ACCESSION	CH230-32M17		DNA sequence.			
VERSION	BH349372.-1		GI:17289106			
KEYWORDS	GSS.					
SOURCE	Rattus norvegicus					
ORGANISM	Rattus norvegicus					
REFERENCE	Zhao,S., Shetty,J., Shatman,S., Tsegaye,G., Geer,K., Shvartsbeyn,Rattus.					
AUTHORS	A., Gebregeorgis,E., Overton,L., Russell,D., Riggs,F., de Jong,P. and Fraser,C.M.					
TITLE	Rat BAC End Sequences from Library CHORI-230 EcorI segment.					
JOURNAL	Unpublished (1999)					
COMMENT	Other_GSS: CH230-32M17.TV					
Contact:	Shayling Zhao					
Department:	Bukarayton Genomics					
The Institute for Genomic Research						
9712 Medical Center Dr., Rockville, MD 20850, USA						
Tel:	301 838 0200					
Fax:	301 838 0208					
Email:	szhao@tigr.org					
Clones are derived from the rat BAC library CHORI-230 ( <a href="http://www.chori.org/bacpac/rat230.htm">http://www.chori.org/bacpac/rat230.htm</a> ). For BAC library availability, please contact Pieter de Jong ( <a href="mailto:pdejong@email.cho.org">pdejong@email.cho.org</a> ). Clones may be purchased from BACPAC Resources ( <a href="http://www.chori.org/bacpac/or_ering_informations.htm">http://www.chori.org/bacpac/or_ering_informations.htm</a> ). BAC end Page: <a href="http://www.tigr.org/tgb/bac_ends/rat/bac_end_intro.html">http://www.tigr.org/tgb/bac_ends/rat/bac_end_intro.html</a>						
Seq primer:	SP6					
Class:	BAC ends.					
FEATURES						
source	Location/Qualifiers					
1.	.499					
/organism="Rattus norvegicus"						
/strain="BN/SSNHSd/NCW"						
/db_xref="Taxon:10116"						
/clone="CH230-32M17"						
/clone_libr="CHORI-230 Segment 1"						
/sex="Female"						
/cell_type="Brain"						
/notext="Vector: PTABRC2.1; Site:1: EcorI; Site:2: EcorI;						
CHORI-230 Rat (BN/SSNHSd/NCW) BAC library produced by						
Pieter de Jong						
BASE COUNT	146 a	123 c	124 g	106 t		
ORIGIN						
REMARK						
COMMENT						
Contact:	MGC Help Desk					
Email:	cabps+@email.nih.gov					
Tissue Procurement:	David N. Louis, M.D.					
CDNA Library Preparation:	Life Technologies, Inc.					
Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA						
NIH MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>						
Sequencing Center:	Baylor College of Medicine Human Genome					
Center code: BCM-HGSC						
Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a>						
Contact:	amg@bcm.tmc.edu					
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,						

clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNBL at: <http://image.llnl.gov>  
Series: INRA Plate: 42 Row: g Column: 16  
This clone has the following problem: no polyA+tail

Source	Features	Location/Qualifiers
1. .3063	/organism="Homo sapiens"	Location has the location field

CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the T.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNLMI699 row: 9 column: 21  
High quality sequence stop: 817.  
Location/Qualifiers

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/tissue_type="Brain, anaplastic oligodendroglioma with
IP/19q loss"
/clone_idb="NCI_CGP_Brn67"
/lab_host="DH10B"
/note_Vector: pCMV-SPORT6"

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</lab> <xref> "taxon:9600"
<clone> "IMAGE:5276572"
<clone_id> "NIH_MGC_95"
<tissue> "hippocampus"
</lab> <host> "DH10B"
<note> "Organ: brain; Vector: pBluescriptTR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XbaI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNTVN-3',
size-selected for average insert size 2.5 kb and

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Query Match		Score	DB ID	Length
Best Local Similarity	Matches	372; 8;	DB 11;	3063;
Conservative	Mismatches	98.2%; 0;	Pred. No.	1.8e-87;
			Indels	Gaps
QY	2019	GGTGGACAACATGATCAAGAGACAACTGGCCATTGGTTGGGGACCCATTCTTGAG        GGTGGACAACATGATCAAGAGACAACTGGCCATTGGTTGGGGACCCATTCTTGAG	2078	0;
DB	1	GGTGGACAACATGATCAAGAGACAACTGGCCATTGGTTGGGGACCCATTCTTGAG        GGTGGACAACATGATCAAGAGACAACTGGCCATTGGTTGGGGACCCATTCTTGAG	60	0;

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library." BASE COUNT ORIGIN

227	a	190	c	237	g	163	t
-----	---	-----	---	-----	---	-----	---

OY	2079	GACCACTTCATGGAGGCCATCACCGTCAGTCAGCAGGGATGAGGTGAGATGATC	2138
Db	61	GGACCACTTCATGGAGGCCATCACCGTCAGTCAGCAGGGATGAGGTGAGATGATC	120
QY	2139	CGGGAGGAGGGCTGCCTCCCTGTTGACTACGTCATGCACTTCCTAGCTGCTCTG	2198
Db	121	CGGGAGGAGGGCTGCCTCCCTGTTGACTACGTCATGCACTTCCTAGCTGCTCTG	180
QY	2199	GAAGGTTGCTTGCGCTGTCGCCAACAGTAACTGACTGTCACGGGGCTGCTGCG	2258
Db	181	GAAGGTTGCTTGCGCTGTCGCCAACAGTAACTGACTGTCACGGGGCTGCTGCG	240
OY	2259	CGCTCCATTCATCATGGCTCACGCCATGTCAGCTGCTCGACT	2318
Db	241	CGCTCCATTCATCATGGCTCACGCCATGTCAGCTGCTCGACT	300
OY	2319	CGGTGCACTATGGTCATCAAGATTCAGTCAGTCAGCTGTTGTTGCTGCACT	2378
Db	301	CGGTGCACTATGGTCATCAAGATTCAGTCAGTCAGCTGTTGCTGCACT	360
OY	2379	CTCTGTCGACCATGGTCATCAAGATTCAGTCAGTCAGCTGTTGCTGCACT	2402
Db	361	CTCTGTCGACCATGGTCATCAAGATTCAGTCAGTCAGCTGTTGCTGCACT	384

RESULT	13
BITSID	BITS1720
DEFINITION	mRNA sequence.
ACCESSION	603191384Fl NIH_MGC_95
VERSION	BITS1720
KEYWORDS	
SOURCE	EST.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 817)
AUTHORS	NIH-MGC <a href="http://mgc.ncbi.nih.gov/">http://mgc.ncbi.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
TISSUE	Procurement: Miklos Palkovits, M.D., Ph.D.
LIBRARY	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Yoshiyuki and Piero Carninci (RIKEN)

QY	2080	GA-CCAGTTCATGGAGGCCATC -ACCGTCAGTCAGCAGGGATG -ACGGATGAGGA -TGA	2135
Db	548	GACCACATTCTAGGAGGCCATCAACCTCTAGTCAGCAGCAGGGATGCAAGGATGAGGATGTA	607
QY	2136	ATCCGGGGAGGA -GAGGCTGCACCTCCGCTCTTGACTA - -CGTCTATGCAGCTCTGTA - CT	2190
Db	608	ATCCGGGGAGGAAGCAGCTGCCTCCCTGCTTGAACATACCGCTCATGCAGCTCTGACCT	667
QY	2191	GCTCTCTGGAA -GGTGTCTGTTGCTCTG TGCCGCCAACAGAGTACTGCACACGCTGGC	2249
Db	668	GCTCTCTGGAAAGGGTCTGTTGCCCTGTGCCACCCAGAGTACTGCACACGCTGGC	727
QY	2250	CTGCTCTGGCTCTCATCTCATCTGCTGCTGCTACCCGCATCATCTGCTGCTGCTGCTGCTG	2308
Db	728	CTGCTCTGGCTCTCATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	787
QY	2309	CCTCGCACTGGCTGACCATGGTCTCAA	2339
Db	788	CCTCGCACTGGCTGACCATGGTCTCAA	817

LOCUS	BG819145	655 bp	mRNA	linear	EST	22-MAY-2001
DEFINITION	602781259F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4932133					
ACCESSION	5', mRNA sequence.					
VERSION	BG819145					
KEYWORDS	5'					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 655)					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert.Strausberg, Ph.D.					
	Email: cgapps:r@mail.nih.gov					
TISSUE	Tissue Procurement: David N. Louis, M.D.					
LIBRARY	cDNA Library Preparation: Life Technologies, Inc.					
PREPARATION	DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)					
ARRAVERED	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov					
BY	Plate: LLM10857 row: g column: 14					
High quality sequence stop: 653.						
FEATURES	1. .655					
SOURCE	location/Qualifiers					
	/organism="Homo sapiens"					
	/db_xref="taxon:9505"					
	/clone_id="NCI_CGAP_Brn67"					
	/tissue_type="anaplastic oligodendrogloma with 1p/19q loss"					
	/lab_host="DHL10B (T1 phage-resistant)"					
	/note="Orgin: Vector; PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."					
BASE COUNT	156 a 168 c 156 g 175 t					
ORIGIN						
	Query Match 13.1%; Score 361.8; DB 12; Length 655:					
	Best Local Similarity 97.9%; Pred. No. 5.9e-85; Mismatches 377; Conservatve 0; Indels 1; Gaps 1;					
BY	2019 GGTGGACAACTAGTCAGTCAAGAACGACAACCTGGCTTGTGGGGACCCATTCTGTGA 2077					
Db	1 GGTGGACAACTAGTCAGTCAAGAACGACAACCTGGCTTGTGGGGACCCATTCTGTGA 60					
Qy	2078 GGAGCAGTCATGGAGGCCATACCGTGAGTGAGCAGAGGGATGAGGATGAAT 2137					
Db	61 GGAGCAGTCATGGAGGCCATACCGTGAGTGAGGATGAGGATGAAT 120					
Qy	2138 CGGGGGAGGGCTGCCCTCTGCTTGACTACAGTCAGTCATGCACTTCTGACTGTCTCT 2197					
Db	121 CGGGGGAGGGCTGCCCTCTGCTTGACTACAGTCATGCACTTCTGACTGTCTCT 180					
Qy	2198 GGAGGGCTGTGTTGCCCTGCTGGCTGCCCTCACAGTAGACTGCACGGCTGGGCTGCTCG 2257					
Db	181 GGAGGGCTGTGTTGCCCTGCCCTCACAGTAGACTGCACGGCTGGGCTGCTCG 240					
Qy	2258 CGCTCTCATCTCATCATGGCATGCTCACGCCCATCATGGACCTGGCTCGACT 2317					
Db	241 CGCTCTCATCTCATCATGGCATGCTCACGCCCATCATGGACCTGGCTCGACT 300					
Qy	2318 TCGGCTGCCACATTGGCTCAAGATTCAGTCACAGCTGTTTCTGGGATTGCCA 2377					
Db	301 TCGGCTGCCACATTGGCTCAAGATTCAGTCACAGCTGTTTCTGGGATTGCCA 360					
Qy	2378 CTCCTGTCACATGAGTGTGCCAG 2402					
Db	361 CTCCTGTCACATGAGTGTGCCAG 385					
FEATURES	1. .655					
SOURCE	location/Qualifiers					
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	/db_xref="IMAGE:4932133"					
	/clone_id="NCI_CGAP_Brn67"					
	/tissue_type="anaplastic oligodendrogloma with 1p/19q loss"					
	/lab_host="DHL10B (T1 phage-resistant)"					
	/note="Orgin: Vector; PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Oligo dT primed. Average insert size: 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."					
BASE COUNT	176 a 183 c 198 g 150 t					
ORIGIN						
	Query Match 13.0%; Score 359.4; DB 12; Length 677:					
	Best Local Similarity 93.3%; Pred. No. 2.6e-84; Mismatches 419; Conservatve 0; Indels 26; Gaps 4; Gaps 4;					
Qy	1785 GAAACCATTAAGGTTAAATAGTAGATGAGGAGGAATACGAAAGGGAGAGATTC 1844					
Db	227 GAAACCATTAAGGTTAAATAGTAGATGAGGAGGAATACGAAAGGGAGAGATTC 286					
Qy	1845 CATGGCTTGGTCAACCGAATGGATGGAACCTGGATATCGATGAGACAGACGAA 1904					
Db	287 CATGGCTTGGTCAACCGAATGGATGGAACCTGGATATCGAGACAGACGAA 346					
Qy	1905 GCTGACTATGGA_AGAAGAGGGCCAAGAGGATGAGAGATGGGAAGGGAGATWT 1962					
Db	347 GCTGACTATGGA_AGAAGAGGGCCAAGAGGATGAGAGATGGGAAGGGAGATWT 406					
Qy	1953 GGTGACACCCCAACTAGAAGTCATCATGTAA-GASTCTATGAGTCAGACTGGT 2081					
Db	407 GTGTGACACCCCAACTAGAAGTCATCATGTAA-GASTCTATGAGTCAGACTGGT 466					
Qy	2022 GGACAACTGATCAGAGACAAACCTGGCTTGGTGTGGGACCCATTCTGGAGGA 2021					
Db	467 GTGTGACACCCCAACTAGAAGTCAGTCACAGCTGAGTCAGACTGGTGTGGGACCCATTCTGGAGGA 526					
Qy	2082 CCAGTTGAGGCCATACCGTCAGTGAGCAGGAGGGATGAGGATGAGGATGAATGCCA 2141					
Db	527 CCAGTTGAGGCCATACCGTCAGTGAGCAGGAGGGATGAGGATGAGGATGAATGCCA 586					

Tue Dec 3 11:07:42 2002

us-10-054-680-1.rst

Qy 2142 GGAGGAGGGCTGCCCTCTGCCTTGACTTACGTCATGCACCTCTGACTCTGACTGTCTCTGGAA 2201  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 587 AGAGGAGGGCTGCCCATCCCTGCTTGACTTACGTCATGCACCTCTGACGGCTCTGGAA 646

Qy 2202 GGCGCTGTTGCCCTGTTGCCCTGGACAG 2230  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 647 GGCTT-CCTGCCCTGTTGCCCTGGACAG 674

Search completed : November 30, 2002, 12:23:11  
Job time : 2560 secs